

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: EVANS, CHRISTOPHER J.
KEITH, DUANE E.
- (ii) TITLE OF INVENTION: OPIOID RECEPTOR GENES
- (iii) NUMBER OF SEQUENCES: 25
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: MORRISON & FOERSTER
 - (B) STREET: 2000 Pennsylvania Avenue, N.W. Suite 5500
 - (C) CITY: Washington
 - (D) STATE: DC
 - (E) COUNTRY: USA
 - (F) ZIP: 20006-1888
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/403,260
 - (B) FILING DATE: 13-MAR-1995
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: MURASHIGE, KATE H.
 - (B) REGISTRATION NUMBER: 29,959
 - (C) REFERENCE/DOCKET NUMBER: 22000-20526.21
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202) 887-1500
 - (B) TELEFAX: (202) 887-0763

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Tyr	Gly	Gly	Phe	Met
1				5

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Tyr Gly Gly Phe Leu
1 5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "D form of amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Tyr Ser Gly Phe Leu Thr
1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 - (B) LOCATION: group(2, 5)
 - (D) OTHER INFORMATION: /product= "OTHER"
- /note= "D-penicillamine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Tyr Xaa Gly Phe Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "D form of amino acid"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "D form of amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Tyr Ala Gly Phe Leu
1 5

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 2
(D) OTHER INFORMATION: /note= "D form of amino acid"

- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 4
(D) OTHER INFORMATION: /product= "MePhe"
/note= "N-Methylphenylalanine"

- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /product= "Gly-ol"
/note= "Carboxy end of glycine has been replaced with an alcohol substituent"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Tyr Ala Gly Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1829 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 29..1144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCACGGTGGGACGACGACG GCGGCGCC ATG GAG CTG GTG CCC TCT GCC CGT	52
Met Glu Leu Val Pro Ser Ala Arg	
1 5	
GCG GAG CTG CAG TCC TCG CCC CTC GTC AAC CTC TCG GAC GCC TTT CCC	100
Ala Glu Leu Gln Ser Ser Pro Leu Val Asn Leu Ser Asp Ala Phe Pro	
10 15 20	
AGC GCC TTC CCC AGC GCG GGC GCC AAT GCG TCG GGG TCG CCG GGA GCC	148
Ser Ala Phe Pro Ser Ala Gly Ala Asn Ala Ser Gly Ser Pro Gly Ala	
25 30 35 40	

CGT	AGT	GCC	TCG	TCC	CTC	GCC	CTA	GCC	ATC	GCC	ATC	ACC	GCG	CTC	TAC	196
Arg	Ser	Ala	Ser	Ser	Leu	Ala	Leu	Ala	Ile	Ala	Ile	Thr	Ala	Leu	Tyr	
				45					50					55		
TCG	GCT	GTG	TGC	GCA	GTG	GGG	CTT	CTG	GGC	AAC	TGT	CTC	GTC	ATG	TTT	244
Ser	Ala	Val	Cys	Ala	Val	Gly	Leu	Leu	Gly	Asn	Cys	Leu	Val	Met	Phe	
			60					65					70			
GGC	ATC	GTC	CGG	TAC	ACC	AAA	TTG	AAG	ACC	GCC	ACC	AAC	ATC	TAC	ATC	292
Gly	Ile	Val	Arg	Tyr	Thr	Lys	Leu	Lys	Thr	Ala	Thr	Asn	Ile	Tyr	Ile	
		75					80					85				
TTC	AAT	CTG	GCT	TTG	GCT	GAT	GCG	CTG	GCC	ACC	AGC	ACG	CTG	CCC	TTC	340
Phe	Asn	Leu	Ala	Leu	Ala	Asp	Ala	Leu	Ala	Thr	Ser	Thr	Leu	Pro	Phe	
	90					95					100					
CAG	AGC	GCC	AAG	TAC	TTG	ATG	GAA	ACG	TGG	CCG	TTT	GGC	GAG	CTG	CTG	388
Gln	Ser	Ala	Lys	Tyr	Leu	Met	Glu	Thr	Trp	Pro	Phe	Gly	Glu	Leu	Leu	
105					110					115					120	
TGC	AAG	GCT	GTG	CTC	TCC	ATT	GAC	TAC	TAC	AAC	ATG	TTC	ACT	AGC	ATC	436
Cys	Lys	Ala	Val	Leu	Ser	Ile	Asp	Tyr	Tyr	Asn	Met	Phe	Thr	Ser	Ile	
				125					130					135		
TTC	ACC	CTC	ACC	ATG	ATG	AGC	GTG	GAC	CGC	TAC	ATT	GCT	GTC	TGC	CAT	484
Phe	Thr	Leu	Thr	Met	Met	Ser	Val	Asp	Arg	Tyr	Ile	Ala	Val	Cys	His	
			140					145					150			
CCT	GTC	AAA	GCC	CTG	GAC	TTC	CGG	ACA	CCA	GCC	AAG	GCC	AAG	CTG	ATC	532
Pro	Val	Lys	Ala	Leu	Asp	Phe	Arg	Thr	Pro	Ala	Lys	Ala	Lys	Leu	Ile	
		155					160					165				
AAT	ATA	TGC	ATC	TGG	GTC	TTG	GCT	TCA	GGT	GTC	GGG	GTC	CCC	ATC	ATG	580
Asn	Ile	Cys	Ile	Trp	Val	Leu	Ala	Ser	Gly	Val	Gly	Val	Pro	Ile	Met	
	170					175					180					
GTC	ATG	GCA	GTG	ACC	CAA	CCC	CGG	GAT	GGT	GCA	GTG	GTA	TGC	ATG	CTC	628
Val	Met	Ala	Val	Thr	Gln	Pro	Arg	Asp	Gly	Ala	Val	Val	Cys	Met	Leu	
185					190					195					200	
CAG	TTC	CCC	AGT	CCC	AGC	TGG	TAC	TGG	GAC	ACT	GTG	ACC	AAG	ATC	TGC	676
Gln	Phe	Pro	Ser	Pro	Ser	Trp	Tyr	Trp	Asp	Thr	Val	Thr	Lys	Ile	Cys	
				205					210					215		
GTG	TTC	CTC	TTT	GCC	TTC	GTG	GTG	CCG	ATC	CTC	ATC	ATC	ACG	GTG	TGC	724
Val	Phe	Leu	Phe	Ala	Phe	Val	Val	Pro	Ile	Leu	Ile	Ile	Thr	Val	Cys	
			220					225					230			
TAT	GGC	CTC	ATG	CTA	CTG	CGC	CTG	CGC	AGC	GTG	CGT	CTG	CTG	TCC	GGT	772
Tyr	Gly	Leu	Met	Leu	Leu	Arg	Leu	Arg	Ser	Val	Arg	Leu	Leu	Ser	Gly	
		235					240					245				
TCC	AAG	GAG	AAG	GAC	CGC	AGC	CTG	CGG	CGC	ATC	ACG	CGC	ATG	GTG	CTG	820
Ser	Lys	Glu	Lys	Asp	Arg	Ser	Leu	Arg	Arg	Ile	Thr	Arg	Met	Val	Leu	
	250					255					260					
GTG	GTG	GTG	GGC	GCC	TTC	GTG	GTG	TGC	TGG	GCG	CCC	ATC	CAC	ATC	TTC	868
Val	Val	Val	Gly	Ala	Phe	Val	Val	Cys	Trp	Ala	Pro	Ile	His	Ile	Phe	
265					270					275					280	
GTC	ATC	GTC	TGG	ACG	CTG	GTG	GAC	ATC	AAT	CGG	CGC	GAC	CCA	CTT	GTG	916
Val	Ile	Val	Trp	Thr	Leu	Val	Asp	Ile	Asn	Arg	Arg	Asp	Pro	Leu	Val	
				285					290					295		

GTG GCC GCA CTG CAC CTG TGC ATT GCG CTG GGC TAC GCC AAC AGC AGC	964
Val Ala Ala Leu His Leu Cys Ile Ala Leu Gly Tyr Ala Asn Ser Ser	
300 305 310	
CTC AAC CCG GTT CTC TAC GCC TTC CTG GAC GAG AAC TTC AAG CGC TGC	1012
Leu Asn Pro Val Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys	
315 320 325	
TTC CGC CAG CTC TGT CGC ACG CCC TGC GGC CGC CAA GAA CCC GGC AGT	1060
Phe Arg Gln Leu Cys Arg Thr Pro Cys Gly Arg Gln Glu Pro Gly Ser	
330 335 340	
CTC CGT CGT CCC CGC CAG GCC ACC ACG CGT GAG CGT GTC ACT GCC TGC	1108
Leu Arg Arg Pro Arg Gln Ala Thr Thr Arg Glu Arg Val Thr Ala Cys	
345 350 355 360	
ACC CCC TCC GAC GGC CCG GGC GGT GGC GCT GCC GCC TGACCTACCC	1154
Thr Pro Ser Asp Gly Pro Gly Gly Gly Ala Ala Ala	
365 370	
GACCTTCCCC TTAAACGCCC CTCCCAAGTG AAGTGATCAG AGGCCACACC GAGCTCCCTG	1214
GGAGGCTGTG GCCACCACCA GGACAGCTAG AATTGGGCCT GCACAGAGGG GAGGCCTCCT	1274
GTGGGGACGG GCCTGAGGGA TCAAAGGCTC CAGGTTGGAA CGGTGGGGGT GAGGAAGCAG	1334
AGCTGGTGAT TCCTAAACTG TATCCATTAG TAAGGCCTCT CAATGGGACA GAGCCTCCGC	1394
CTTGAGATAA CATCGGGTTC TGGCCTTTTT GAACACCCAG CTCCAGTCCA AGACCCAAGG	1454
ATTCCAGCTC CAGAACCAGG AGGGGCAGTG ATGGGGTCGA TGATTTGGTT TGGCTGAGAG	1514
TCCCAGCATT TGTGTTATGG GGAGGATCTC TCATCTTAGA GAAGAAAGGG GACAGGGCAT	1574
TCAGGCAAGG CAGCTTGGGG TTTGGTCAGG AGATAAGCGC CCCCCTTCCC TTGGGGGGAG	1634
GATAAGTGGG GGATGGTCAC GTTGGAGAAG AGTCAAAGTT CTCACCACCT TTCTAACTAC	1694
TCAGCTAAAC TCGTTGAGGC TAGGGCCAAC GTGACTTCTC TGTAGAGAGG TACAAGCCGG	1754
GCCTGATGGG GCAGGCCTGT GTAATCCCAG TCATAGTGGA GGCTGAGGCT GGAAAATTAA	1814
GGACCAACAG CCCGG	1829

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Glu Leu Val Pro Ser Ala Arg Ala Glu Leu Gln Ser Ser Pro Leu
1 5 10 15
Val Asn Leu Ser Asp Ala Phe Pro Ser Ala Phe Pro Ser Ala Gly Ala
20 25 30
Asn Ala Ser Gly Ser Pro Gly Ala Arg Ser Ala Ser Ser Leu Ala Leu
35 40 45

Ala Ile Ala Ile Thr Ala Leu Tyr Ser Ala Val Cys Ala Val Gly Leu
50 55 60

Leu Gly Asn Cys Leu Val Met Phe Gly Ile Val Arg Tyr Thr Lys Leu
65 70 75 80

Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu Ala Leu Ala Asp Ala
85 90 95

Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Ala Lys Tyr Leu Met Glu
100 105 110

Thr Trp Pro Phe Gly Glu Leu Leu Cys Lys Ala Val Leu Ser Ile Asp
115 120 125

Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu Thr Met Met Ser Val
130 135 140

Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys Ala Leu Asp Phe Arg
145 150 155 160

Thr Pro Ala Lys Ala Lys Leu Ile Asn Ile Cys Ile Trp Val Leu Ala
165 170 175

Ser Gly Val Gly Val Pro Ile Met Val Met Ala Val Thr Gln Pro Arg
180 185 190

Asp Gly Ala Val Val Cys Met Leu Gln Phe Pro Ser Pro Ser Trp Tyr
195 200 205

Trp Asp Thr Val Thr Lys Ile Cys Val Phe Leu Phe Ala Phe Val Val
210 215 220

Pro Ile Leu Ile Ile Thr Val Cys Tyr Gly Leu Met Leu Leu Arg Leu
225 230 235 240

Arg Ser Val Arg Leu Leu Ser Gly Ser Lys Glu Lys Asp Arg Ser Leu
245 250 255

Arg Arg Ile Thr Arg Met Val Leu Val Val Val Gly Ala Phe Val Val
260 265 270

Cys Trp Ala Pro Ile His Ile Phe Val Ile Val Trp Thr Leu Val Asp
275 280 285

Ile Asn Arg Arg Asp Pro Leu Val Val Ala Ala Leu His Leu Cys Ile
290 295 300

Ala Leu Gly Tyr Ala Asn Ser Ser Leu Asn Pro Val Leu Tyr Ala Phe
305 310 315 320

Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Gln Leu Cys Arg Thr Pro
325 330 335

Cys Gly Arg Gln Glu Pro Gly Ser Leu Arg Arg Pro Arg Gln Ala Thr
340 345 350

Thr Arg Glu Arg Val Thr Ala Cys Thr Pro Ser Asp Gly Pro Gly Gly
355 360 365

Gly Ala Ala Ala
370

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 369 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Glu	Leu	Thr	Ser	Glu	Gln	Phe	Asn	Gly	Ser	Gln	Val	Trp	Ile	Pro	1	5	10	15
Ser	Pro	Phe	Asp	Leu	Asn	Gly	Ser	Leu	Gly	Pro	Ser	Asn	Gly	Ser	Asn	20	25	30	
Gln	Thr	Glu	Pro	Tyr	Tyr	Asp	Met	Thr	Ser	Asn	Ala	Val	Leu	Thr	Phe	35	40	45	
Ile	Tyr	Phe	Val	Val	Cys	Val	Val	Gly	Leu	Cys	Gly	Asn	Thr	Leu	Val	50	55	60	
Ile	Tyr	Val	Ile	Leu	Arg	Tyr	Ala	Lys	Met	Lys	Thr	Ile	Thr	Asn	Ile	65	70	75	
Tyr	Ile	Leu	Asn	Leu	Ala	Ile	Ala	Asp	Glu	Leu	Phe	Met	Leu	Gly	Leu	85	90	95	
Pro	Phe	Leu	Ala	Met	Gln	Val	Ala	Leu	Val	His	Trp	Pro	Phe	Gly	Lys	100	105	110	
Ala	Ile	Cys	Arg	Val	Val	Met	Thr	Val	Asp	Gly	Ile	Asn	Gln	Phe	Thr	115	120	125	
Ser	Ile	Phe	Cys	Leu	Thr	Val	Met	Ser	Ile	Asp	Arg	Tyr	Leu	Ala	Val	130	135	140	
Val	His	Pro	Ile	Lys	Ser	Ala	Lys	Trp	Arg	Arg	Pro	Arg	Thr	Ala	Lys	145	150	155	
Met	Ile	Asn	Val	Ala	Val	Trp	Gly	Val	Ser	Leu	Leu	Val	Ile	Leu	Pro	165	170	175	
Ile	Met	Ile	Tyr	Ala	Gly	Leu	Arg	Ser	Asn	Gln	Trp	Gly	Arg	Ser	Ser	180	185	190	
Cys	Thr	Ile	Asn	Trp	Pro	Gly	Glu	Ser	Gly	Ala	Trp	Tyr	Thr	Gly	Phe	195	200	205	
Ile	Ile	Tyr	Ala	Phe	Ile	Leu	Gly	Phe	Leu	Val	Pro	Leu	Thr	Ile	Ile	210	215	220	
Cys	Leu	Cys	Tyr	Leu	Phe	Ile	Ile	Ile	Lys	Val	Lys	Ser	Ser	Gly	Ile	225	230	235	
Arg	Val	Gly	Ser	Ser	Lys	Arg	Lys	Lys	Ser	Glu	Lys	Lys	Val	Thr	Arg	245	250	255	
Met	Val	Ser	Ile	Val	Val	Ala	Val	Phe	Ile	Phe	Cys	Trp	Leu	Pro	Phe	260	265	270	
Tyr	Ile	Phe	Asn	Val	Ser	Ser	Val	Ser	Val	Ala	Ile	Ser	Pro	Thr	Pro	275	280	285	
Ala	Leu	Lys	Gly	Met	Phe	Asp	Phe	Val	Val	Ile	Leu	Thr	Tyr	Ala	Asn	290	295	300	

Ser Cys Ala Asn Pro Ile Leu Tyr Ala Phe Leu Ser Asp Asn Phe Lys
 305 310 315 320
 Lys Ser Phe Gln Asn Val Leu Cys Leu Val Lys Val Ser Gly Ala Glu
 325 330 335
 Asp Gly Glu Arg Ser Asp Ser Lys Gln Asp Lys Ser Arg Leu Asn Glu
 340 345 350
 Thr Thr Glu Thr Gln Arg Thr Leu Leu Asn Gly Asp Leu Gln Thr Ser
 355 360 365
 Ile

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 130 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGCAGTGGT GTGCATGCTC CAGTTCCCCA GCCCCAGCTG GTACTGGGAC ACGGTGACCA 60
 AGATCTGCGT GTTCCTCTTC GCCTTCGTGG TGCCCATCCT CATCATCACC GTGTGCTATG 120
 GCCTCATGCT 130

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 130 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGTGCAGTGG TATGCATGCT CCAGTTCCCC AGTCCCAGCT GGTACTGGGA CACTGTGACC 60
 AAGATCTGCG TGTTCTCTT TGCCTTCGTG GTGCCGATCC TCATCATCAC GGTGTGCTAT 120
 GGCCTCATGC 130

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2447 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCTGGCCTTT TGGGGATGTG CTGTGCAAGA TAGTAATTTT CATTGATTAC TACAACATGT 60
 TCACCAGCAT CTTACCTTG ACCATGATGA GCGTGGACCG CTACATTGCC GTGTGCCACC 120
 CCGTGAAGGC TTTGGACTTC CGCACACCCT TGAAGGCAAA GATCATCAAT ATCTGCATCT 180

GGCTGCTGTC	GTCATCTGTT	GGCATCTCTG	CAATAGTCCT	TGGAGGCACC	AAAGTCAGGG	240
AAGGTAAGAG	CAGTCATTTT	ATTCTGTTCA	TAAAAATGTA	GCTTCAAATT	ACATAGACTT	300
TTAATTTGAG	CGTGAGTAGG	CCACATATTT	GTGGAAATCG	ATGCCAAAAG	ACGACGGAAA	360
TGTAGTGCCT	AAATCCATGG	AAGATGAGAA	GTAGAACAAT	TTTTTGTCCC	TTCCACCTC	420
TAAACACAGA	ATGCAATAAT	GACATTGCCA	GAAGAGAGAT	GCCCCACCTG	TCTCCCATT	480
TGGCAATGTT	TAGTAGAAAG	TGGAGGGGTG	AGGATGAGGT	AAGAACCACA	GGCATGTAGA	540
TTTTAAAGTA	CAACCTGGCA	AGTCCAGACA	CACCTTCTCA	CTCCTTTTTT	TCTCTTTAAC	600
AAGGGATATA	AATTATTGGT	GACATATGCT	GGTTGTTTCC	TCTTTTATT	CTAAAGGATA	660
ACCTCCAAAT	CACTATTTTA	ACAGCTTTGG	CGTAGGATCT	CAAAATCAAG	TTAACGGATG	720
GTAGTTACAG	ATGAGTCAGA	ACCACTTGAT	TTGGACATAT	CAGGTTTTCC	CTTGCAAACC	780
AGCCAACTGA	TTTTTTTTTT	TTTTTTTTTT	GAGAGAGAGT	CTTGCTCTGT	TGCCAGGCTA	840
GAGTGCAGTG	GCGCGATATC	GGCTCACTGC	AACCTCTGCC	TCCCGGGTTC	AACCTCAGCC	900
TCTCGAGTAG	CTGGGACTAC	TGGCACACAC	CACCATGCCC	AGCTAATTTT	TGTATTTTTA	960
GTAGAGACAG	GGTTTCACCG	TGTTGGCCAG	GGTGGTCTCA	ATCTCTTGAC	CTCGTGATCT	1020
GCCCGCCTCG	NCTCCCCAAA	GTGCTGGGAT	TACAGGCGTG	CNCTGCNCCC	GNCCCCTGTT	1080
GATGTTTTTC	CTGTATTTCT	AGGACAGTAG	TTCTCACTCT	GGGCTGCACA	TTGGAATCAC	1140
CTGGGTACTT	TAGAAAACAC	TGCTGCCTGC	ATCCCACCCC	TTAAGGGTCT	GGTGTAATTG	1200
ACCTGGGGTA	CAGCCTGGGT	GTCAAGATTT	TTGAGCTCTC	TCCAGGTGAC	TCTGACCTGC	1260
AGCCAAGGTG	AGAGGTACTG	TTCTAGGAGT	TTTGCTTTAC	TAGCAAAATA	TAAAGCTATA	1320
GAAAGCATCT	TTTGTTCCCT	ATAGAAATTA	ATGATGGGGA	GGTGAGCAGA	ATAGTCACTC	1380
TGGGCCTACT	CATGCTGTTT	AATGCTCCAG	CAGGTATATA	GGTTCTCCAG	TTACTAGGGG	1440
GTTCATAATA	CCTGTGAGAG	CAGATAACTG	AGTGTATATA	GTGAGGATTT	CCAGGTCATA	1500
GTGAAAGGGC	AAGGCACTAA	AATCATAGCT	TGTCTTGCAT	ATACTGTTTG	TTTGTTTTTA	1560
GACTTACATG	TTAGGTTTCA	GTTTACGTTT	TAGGTTTACA	GCAAACTGA	CCAGAAAGCA	1620
CAGAGAGGCA	CTTCNATTTA	CCTCCATTTA	CCCCACACAG	GCACATCCTC	CCCTACAGAG	1680
TGGTCCATTT	ATTACAGCTG	CTGAACCCAC	ACTGACACGC	TGTTATCACT	CAGAGCCTGG	1740
CAGTTTACAG	AGGCTCACTC	TCCGNTATGT	GTCCTGTGNT	TTGAACAAAT	GTATAATGAC	1800
TTTATTCATT	GTTTTTTAAT	GAAGCTGATC	TTTTCCCTCT	GAAACTACAA	AATGAATTTT	1860
TAGCATAGCC	ATAGCAGGTG	TCAAGCTATA	CTACTAGGTA	AATTTTAAGA	AATGCCCAAC	1920
TTTATCATAT	TTGCATTTCA	AAATATGATT	AATCACACAT	AGGATTTTGT	TTCTTCATGC	1980
CTACAGCAAA	TAGAAATAAA	GTGCAAGAAA	CTTTTCTGAG	GCAAAGCTTT	CACTTTGTGA	2040
ACGTAAATG	TTGACTCTAA	TATTTTCCAT	ACTGTAGTAT	ATGTGTGTGT	ATTATGTGAG	2100
GATTCATAGT	CTGCTCTTAC	TTTTTTATAG	TAGCTAAGAA	TTATTATAAT	CGCTATAAGC	2160

AGAAACAATT ATTCTTAACA AAATGAATAC ACACAAGAAA AGCTTTAGTT TAGCTATTAG	2220
AACTAACTCT ATAATTATGA TAACCATGAG ATGCTGGAAC AGGAGCCAGC AGAAGCCACA	2280
GCCCTCTGAT ATTAATATAT AAAGAAACCA AAATCTGCTT GTTAAACTGA GGCAGTTGTA	2340
TGGATACTTC AACCTGAAAA TGCCCCCTTC TTCCTGAAAC AGAACATTTA ATAAAAATGG	2400
CATGCTTGGA CAGGAATTTT TTTTTTAAAA AATGCTTAGT TTTTATG	2447

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 830 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTCCTTTATC TCCTAGATAC ACCAAGATGA AGACTGCCAC CAACATCTAC ATTTTCAACC	60
TTGCTCTGCA GATGCCTTAG CCACCAGTAC CCTGCCCTTC CAGAGTGTGA ATTACCTAAT	120
GGGAACATGG CCATTGGAA CCATCCTTTG CAAGATAGTG ATCTCCATAG ATTACTATAA	180
CATGTTTACC AGCATATTCA CCCTCTGCAC CATGAGTGTT GATCGATACA TTGCAGTCTG	240
CCACCCTGTC AAGGCCTTAG ATTTCCGTAC TCCCCNNNNN NNNNNNNNNN NNNNNNNNNN	300
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	360
NNNNNNNNNGT TCCATAGATT GTACACTAAC ATTCTCTCAT CCAACCTGGT ACTGGGAAAA	420
CCTGCTGAAG ATCTGTGTTT TCATCTTCGC CTTCAATTATG CCAGTGCTCA TCATTACCGT	480
GTGCTATGGA CTGATGATCT TGCGCCTCAA GAGTGTCCGC ATGCTCTCTG GCTCCAAAGA	540
AAAGGACAGG AATCTTCGAA GGATCACCAG GATGGTGCTG GTGGTGGTGG CTGTGTTTAT	600
CGTCTGCTGG ACTCCCATTC ACATTTACGT CATCATTAAA GCCTTGGTTA CAATCCCAGA	660
AACTACGTTT CAGACTGTTT CTTGGCACTT CTGCATTGCT CTAGGTTACA CAAACAGCTG	720
CCTCAACCCA GTCCTTTATG CATTTCTGGA TGAAAACTTC CACGATGCTT CAGAGAGTTC	780
TGTATCCCAA CCTCTTCCAA CATTGAGCAA CAAAACCTCA CTCGAATTCC	830

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGGTACCGGG CCCCCCTCG AGGTCGACGG TATCGATAAG CTTGATATCG AATTCTTACT	60
GAATTAGGTA TCTTTCTTCA CACTACTTGG TAAAAAAAT GAAAAGGCAG AAAAATTAGC	120
CCCAAAGAG ATGAAACTCT TCCGTCCATC ACCATTGACT CTATTGTGAA CTTATGAAAA	180

AGGTAGTTGA GCAATATGAA GGCCATGATG TGGAATTAAA CACACACACA CACACACACA	240
CACACACACA CACATGCTGG ATTCTAAATG TGTCCTTCCT CCTCTCACTC TCTTGATTCA	300
AGTTTATTTT TGAAGTGA CACGATCACC AC	332

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1981 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGGATCCTTA GCATCCCCAA AGCGCCTCCG TGTACTTCTA AGGTGGGAGG GGGATACAAG	60
CAGAGGAGAA TATCGGACGC TCAGACGTTT CATTCTGCCT GCCGCTCTTC TCTGGTTCCA	120
CTAGGGCTTG TCCTTGTAAG AAAGTACGG AGCCTAGGGC AGCTGTGAGA GGAAGAGGCT	180
GGGGCGCCTG GAACCCGAAC ACTCTTGAGT GCTCTCAGTT ACAGNCTACC GAGTCCGCAG	240
GAAGCATTCA GAACCATGGA CAGCAGCGCC GGCCCAGGGA ACATCAGCGA CTGCTCTGAC	300
CCCTTAGCTC CTGCAAGTTG CTCCCCAGCA CCTGGCTCCT GGCTCAACTT GTCCACGTT	360
GATGGAAACC AGTCCGACCC ATGCGGTCCT AAGCCGACGG GCCTTGGCGG GAACGACAGC	420
CTGTGCCCTC AGACCGGCAG CCCTTCCATG GTCACAGCCA TCACCATCAT GGCCCTCTAT	480
TCTATCGTGT GTGTAGTGGG CCTCTTTGGA AACTTCCTGG TCATGTATGT GATTGTGAAGA	540
TATACCAAAA TGAAGACTGC CACCAACATC TACATTTTCA ACCTTGCTCT GGCAGATGCC	600
TTAGCCACTA GCACGCTGCC CTTTCAGAGT GTTAACTACC TGATGGGAAC GTGGCCCTTT	660
GGAAACATCC TCTGCAAGAT CGTGATCTCA ATAGACTACT ACAACATGTT CACCAGTATC	720
TTCACCCTCT GCACCATGAG TGTAGACCGC TACATTGCCG TCTGCCACCC GGTCAAGGCC	780
CTGGATTTCC GTACCCCCCG AAATGCCAAA ATTGTCAATG TCTGCAACTG GATCCTCTCT	840
TCTGCCATTG GTCTGCCCCG AATGTTTCATG GCAACCACAA AATACAGGCA GGGGTCCATA	900
GATTGCACCC TCACGTTCTC TCATCCACA TGGTACTGGG AGAACCTGCT CAAAATCTGT	960
GTCTTCATCT TCGCCTTCAT CATGCCGGGC CTCATCATCA CTGTGTGTTA TGGACTGATG	1020
ATCTTACAGC TCAAGAGTGT CCGCATGCTG TCGGGCTCCA AAGAAAAGGA CAGGAACCTG	1080
CGCAGGATCA CCCGGATGGT GCTGGTGGTC GTGGCTGTAT TTATTGTCTG CTGGACCCCC	1140
ATCCACATCT ATGTCATCAT CAAAGCACTG ATCACGATTC CAGAAACCAC TTTCCAGACT	1200
GTTTCCTGGC ACTTCTGCAT TGCCTTGGGT TACACAAACA GCTGCCTGAA CCCAGTTCTT	1260
TATGCGTTCC TGGATGAAAA CTTCAAACGA TGTTTTAGAG AGTTCTGCAT CCCAACTTCC	1320
TCCACAATCG AACAGCAAAA CTCTGCTCGA ATCCGTCAAA AACTAGGGA ACACCCCTCC	1380
ACGGCTAATA CAGTGGATCG AACTAACCAC CAGCTAGAAA ATCTGGAAGC AGAAACTGCT	1440
CCATTGCCCT AACTGGGTCC CACGCCATCC AGACCCTCGC TAAACTTAGA GGCTGCCATC	1500

TACTTGGAAT CAGGTTGCTG TCAGGGTTTG TGGGAGGCTC TGGTTTCCTG GAAAAGCATC	1560
TGATCCTGCA TCATTCAAAG TCATTCCTCT CTGGCTATTC ACGCTACACG TCAGAGACAC	1620
TCAGACTGTG TCAAGCACTC AGAAGGAAGA GACTGCAGGC CACTACTGAA TCCAGCTCAT	1680
GTACAGAAAC ATCCAATGGA CCACAATACT CTGTGGTATG TGATTTGTGA TCAACATAGA	1740
AGGTGACCCT TCCCTATGTG GAATTTTAA TTTCAAGGAA ATACTTATGA TCTCATCAAG	1800
GGAAAAATAG ATGTCACCTG TTAAATTCAC TGTAGTGATG CATAAAGGAA AAGCTACCTC	1860
TGACCTCTAG CCCAGTCACC CTCTATGGAA AGTTCCATAG GGAATATGTG AGGGAAAATG	1920
TTGCTTCCAA ATTAAATTTT CACCTTTATG TTATAGTCTA GTTAAGACAT CAGGGGCATC	1980
T	1981

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 398 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met	Asp	Ser	Ser	Thr	Gly	Pro	Gly	Asn	Thr	Ser	Asp	Cys	Ser	Asp	Pro	1	5	10	15
Leu	Ala	Gln	Ala	Ser	Cys	Ser	Pro	Ala	Pro	Gly	Ser	Trp	Leu	Asn	Leu	20	25	30	
Ser	His	Val	Asp	Gly	Asn	Gln	Ser	Asp	Pro	Cys	Gly	Leu	Asn	Arg	Thr	35	40	45	
Gly	Leu	Gly	Gly	Asn	Asp	Ser	Leu	Cys	Pro	Gln	Thr	Gly	Ser	Pro	Ser	50	55	60	
Met	Val	Thr	Ala	Ile	Thr	Ile	Met	Ala	Leu	Tyr	Ser	Ile	Val	Cys	Val	65	70	75	80
Val	Gly	Leu	Phe	Gly	Asn	Phe	Leu	Val	Met	Tyr	Val	Ile	Val	Arg	Tyr	85	90	95	
Thr	Lys	Met	Lys	Thr	Ala	Thr	Asn	Ile	Tyr	Ile	Phe	Asn	Leu	Ala	Leu	100	105	110	
Ala	Asp	Ala	Leu	Ala	Thr	Ser	Thr	Leu	Pro	Phe	Gln	Ser	Val	Asn	Tyr	115	120	125	
Leu	Met	Gly	Thr	Trp	Pro	Phe	Gly	Thr	Ile	Leu	Cys	Lys	Ile	Val	Ile	130	135	140	
Ser	Ile	Asp	Tyr	Tyr	Asn	Met	Phe	Thr	Ser	Ile	Phe	Thr	Leu	Cys	Thr	145	150	155	160
Met	Ser	Val	Asp	Arg	Tyr	Ile	Ala	Val	Cys	His	Pro	Val	Lys	Ala	Leu	165	170	175	
Asp	Phe	Arg	Thr	Pro	Arg	Asn	Ala	Lys	Ile	Val	Asn	Val	Cys	Asn	Trp	180	185	190	

Ile	Leu	Ser	Ser	Ala	Ile	Gly	Leu	Pro	Val	Met	Phe	Met	Ala	Thr	Thr
		195					200					205			
Lys	Tyr	Arg	Gln	Gly	Ser	Ile	Asp	Cys	Thr	Leu	Thr	Phe	Ser	His	Pro
	210					215					220				
Thr	Trp	Tyr	Trp	Glu	Asn	Leu	Leu	Lys	Ile	Cys	Val	Phe	Ile	Phe	Ala
225					230					235					240
Phe	Ile	Met	Pro	Ile	Leu	Ile	Ile	Thr	Val	Cys	Tyr	Gly	Leu	Met	Ile
				245					250					255	
Leu	Arg	Leu	Lys	Ser	Val	Arg	Met	Leu	Ser	Gly	Ser	Lys	Glu	Lys	Asp
			260					265					270		
Arg	Asn	Leu	Arg	Arg	Ile	Thr	Arg	Met	Val	Leu	Val	Val	Val	Ala	Val
		275					280					285			
Phe	Ile	Val	Cys	Trp	Thr	Pro	Ile	His	Ile	Tyr	Val	Ile	Ile	Lys	Ala
	290					295					300				
Leu	Ile	Thr	Ile	Pro	Glu	Thr	Thr	Phe	Gln	Thr	Val	Ser	Trp	His	Phe
305					310					315					320
Cys	Ile	Ala	Leu	Gly	Tyr	Thr	Asn	Ser	Cys	Leu	Asn	Pro	Val	Leu	Tyr
				325					330					335	
Ala	Phe	Leu	Asp	Glu	Asn	Phe	Lys	Arg	Cys	Phe	Arg	Glu	Phe	Cys	Ile
			340					345					350		
Pro	Thr	Ser	Ser	Thr	Ile	Glu	Gln	Gln	Asn	Ser	Thr	Arg	Val	Arg	Gln
		355					360					365			
Asn	Thr	Arg	Glu	His	Pro	Ser	Thr	Ala	Asn	Thr	Val	Asp	Arg	Thr	Asn
	370					375					380				
His	Gln	Leu	Glu	Asn	Leu	Glu	Ala	Glu	Thr	Ala	Pro	Leu	Pro		
385					390					395					

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met 1	Glu	Ser	Pro	Ile 5	Gln	Ile	Phe	Arg	Gly 10	Asp	Pro	Gly	Pro	Thr 15	Cys
Ser	Pro	Ser	Ala 20	Cys	Leu	Leu	Pro	Asn 25	Ser	Ser	Ser	Trp	Phe 30	Pro	Asn
Trp	Ala	Glu 35	Ser	Asp	Ser	Asn	Gly 40	Ser	Val	Gly	Ser	Glu 45	Asp	Gln	Gln
Leu	Glu 50	Ser	Ala	His	Ile	Ser 55	Pro	Ala	Ile	Pro	Val 60	Ile	Ile	Thr	Ala
Val 65	Tyr	Ser	Val	Val	Phe 70	Val	Val	Gly	Leu 75	Val	Gly	Asn	Ser	Leu 80	Val

Met	Phe	Val	Ile	Ile	Arg	Tyr	Thr	Lys	Met	Lys	Thr	Ala	Thr	Asn	Ile	
				85					90					95		
Tyr	Ile	Phe	Asn	Leu	Ala	Leu	Ala	Asp	Ala	Leu	Val	Thr	Thr	Thr	Met	
			100					105					110			
Pro	Phe	Gln	Ser	Ala	Val	Tyr	Leu	Met	Asn	Ser	Trp	Pro	Phe	Gly	Asp	
			115				120					125				
Val	Leu	Cys	Lys	Ile	Val	Ile	Ser	Ile	Asp	Tyr	Tyr	Asn	Met	Phe	Thr	
	130					135					140					
Ser	Ile	Phe	Thr	Leu	Thr	Met	Met	Ser	Val	Asp	Arg	Tyr	Ile	Ala	Val	
145					150					155					160	
Cys	His	Pro	Val	Lys	Ala	Leu	Asp	Phe	Arg	Thr	Pro	Leu	Lys	Ala	Lys	
				165					170					175		
Ile	Ile	Asn	Ile	Cys	Ile	Trp	Leu	Leu	Ala	Ser	Ser	Val	Gly	Ile	Ser	
			180					185					190			
Ala	Ile	Val	Leu	Gly	Gly	Thr	Lys	Val	Arg	Glu	Asp	Val	Ile	Glu	Cys	
		195					200					205				
Ser	Leu	Gln	Phe	Pro	Asp	Asp	Glu	Trp	Trp	Asp	Leu	Phe	Met	Lys	Ile	
	210					215					220					
Cys	Val	Phe	Val	Phe	Ala	Phe	Val	Ile	Pro	Val	Leu	Ile	Ile	Ile	Val	
225					230					235					240	
Cys	Tyr	Thr	Leu	Met	Ile	Leu	Arg	Leu	Lys	Ser	Val	Arg	Leu	Leu	Ser	
				245					250					255		
Gly	Ser	Arg	Glu	Lys	Asp	Arg	Asn	Leu	Arg	Arg	Ile	Thr	Lys	Leu	Val	
			260					265					270			
Leu	Val	Val	Val	Ala	Val	Phe	Ile	Ile	Cys	Trp	Thr	Pro	Ile	His	Ile	
		275					280					285				
Phe	Ile	Leu	Val	Glu	Ala	Leu	Gly	Ser	Thr	Ser	His	Ser	Thr	Ala	Ala	
	290					295					300					
Leu	Ser	Ser	Tyr	Tyr	Phe	Cys	Ile	Ala	Leu	Gly	Tyr	Thr	Asn	Ser	Ser	
305					310					315					320	
Leu	Asn	Pro	Val	Leu	Tyr	Ala	Phe	Leu	Asp	Glu	Asn	Phe	Lys	Arg	Cys	
				325					330					335		
Phe	Arg	Asp	Phe	Cys	Phe	Pro	Ile	Lys	Met	Arg	Met	Glu	Arg	Gln	Ser	
			340					345					350			
Thr	Asn	Arg	Val	Arg	Asn	Thr	Val	Gln	Asp	Pro	Ala	Ser	Met	Arg	Asp	
		355					360					365				
Val	Gly	Gly	Met	Asn	Lys	Pro	Val									
	370					375										

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1805 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 10..1119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGCAGTGGC ATG GAG CCC CTC TTC CCC GCG CCG TTC TGG GAG GTT ATC	48
Met Glu Pro Leu Phe Pro Ala Pro Phe Trp Glu Val Ile	
375 380 385	
TAC GGC AGC CAC CTT CAG GGC AAC CTG TCC CTC CTG AGC CCC AAC CAC	96
Tyr Gly Ser His Leu Gln Gly Asn Leu Ser Leu Leu Ser Pro Asn His	
390 395 400	
AGT CTG CTG CCC CCG CAT CTG CTG CTC AAT GCC AGC CAC GGC GCC TTC	144
Ser Leu Leu Pro Pro His Leu Leu Leu Asn Ala Ser His Gly Ala Phe	
405 410 415	
CTG CCC CTC GGG CTC AAG GTC ACC ATC GTG GGG CTC TAC CTG GCC GTG	192
Leu Pro Leu Gly Leu Lys Val Thr Ile Val Gly Leu Tyr Leu Ala Val	
420 425 430	
TGT GTC GGA GGG CTC CTG GGG AAC TGC CTT GTC ATG TAC GTC ATC CTC	240
Cys Val Gly Gly Leu Leu Gly Asn Cys Leu Val Met Tyr Val Ile Leu	
435 440 445	
AGG CAC ACC AAA ATG AAG ACA GCC ACC AAT ATT TAC ATC TTT AAC CTG	288
Arg His Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu	
450 455 460 465	
GCC CTG GCC GAC ACT CTG GTC CTG CTG ACG CTG CCC TTC CAG GGC ACG	336
Ala Leu Ala Asp Thr Leu Val Leu Leu Thr Leu Pro Phe Gln Gly Thr	
470 475 480	
GAC ATC CTC CTG GGC TTC TGG CCG TTT GGG AAT GCG CTG TGC AAG ACA	384
Asp Ile Leu Leu Gly Phe Trp Pro Phe Gly Asn Ala Leu Cys Lys Thr	
485 490 495	
GTC ATT GCC ATT GAC TAC TAC AAC ATG TTC ACC AGC ACC TTC ACC CTA	432
Val Ile Ala Ile Asp Tyr Tyr Asn Met Phe Thr Ser Thr Phe Thr Leu	
500 505 510	
ACT GCC ATG AGT GTG GAT CGC TAT GTA GCC ATC TGC CAC CCC ATC CGT	480
Thr Ala Met Ser Val Asp Arg Tyr Val Ala Ile Cys His Pro Ile Arg	
515 520 525	
GCC CTC GAC GTC CGC ACG TCC AGC AAA GCC CAG GCT GTC AAT GTG GCC	528
Ala Leu Asp Val Arg Thr Ser Ser Lys Ala Gln Ala Val Asn Val Ala	
530 535 540 545	
ATC TGG GCC CTG GCC TCT GTT GTC GGT GTT CCC GTT GCC ATC ATG GGC	576
Ile Trp Ala Leu Ala Ser Val Val Gly Val Pro Val Ala Ile Met Gly	
550 555 560	
TCG GCA CAG GTC GAG GAT GAA GAG ATC GAG TGC CTG GTG GAG ATC CCT	624
Ser Ala Gln Val Glu Asp Glu Glu Ile Glu Cys Leu Val Glu Ile Pro	
565 570 575	
ACC CCT CAG GAT TAC TGG GGC CCG GTG TTT GCC ATC TGC ATC TTC CTC	672
Thr Pro Gln Asp Tyr Trp Gly Pro Val Phe Ala Ile Cys Ile Phe Leu	
580 585 590	
TTC TCC TTC ATC GTC CCC GTG CTC GTC ATC TCT GTC TGC TAC AGC CTC	720
Phe Ser Phe Ile Val Pro Val Leu Val Ile Ser Val Cys Tyr Ser Leu	
595 600 605	

ATG ATC CGG CGG CTC CGT GGA GTC CGC CTG CTC TCG GGC TCC CGA GAG Met Ile Arg Arg Leu Arg Gly Val Arg Leu Leu Ser Gly Ser Arg Glu 610 615 620 625	768
AAG GAC CGG AAC CTG CGG CGC ATC ACT CGG CTG GTG CTG GTG GTA GTG Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Leu Val Leu Val Val Val 630 635 640	816
GCT GTG TTC GTG GGC TGC TGG ACG CCT GTC CAG GTC TTC GTG CTG GCC Ala Val Phe Val Gly Cys Trp Thr Pro Val Gln Val Phe Val Leu Ala 645 650 655	864
CAA GGG CTG GGG GTT CAG CCG AGC AGC GAG ACT GCC GTG GCC ATT CTG Gln Gly Leu Gly Val Gln Pro Ser Ser Glu Thr Ala Val Ala Ile Leu 660 665 670	912
CGC TTC TGC ACG GCC CTG GGC TAC GTC AAC AGC TGC CTC AAC CCC ATC Arg Phe Cys Thr Ala Leu Gly Tyr Val Asn Ser Cys Leu Asn Pro Ile 675 680 685	960
CTC TAC GCC TTC CTG GAT GAG AAC TTC AAG GCC TGC TTC CGC AAG TTC Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Ala Cys Phe Arg Lys Phe 690 695 700 705	1008
TGC TGT GCA TCT GCC CTG CGC CGG GAC GTG CAG GTG TCT GAC CGC GTG Cys Cys Ala Ser Ala Leu Arg Arg Asp Val Gln Val Ser Asp Arg Val 710 715 720	1056
CGC AGC ATT GCC AAG GAC GTG GCC CTG GCC TGC AAG ACC TCT GAG ACG Arg Ser Ile Ala Lys Asp Val Ala Leu Ala Cys Lys Thr Ser Glu Thr 725 730 735	1104
GTA CCG CGG CCC GCA TGA CTAGGCG TGGACCTGCC CATGGTGCCT GTCAGCCCGC Val Pro Arg Pro Ala 740	1159
AGAGCCCATC TACGCCCAAC ACAGAGCTCA CACAGGTCAC TGCTCTCTAG GCGGACACAC	1219
CCTGGGGCCCT GAGCATCCAG AGCCTGGGAT GGGCTTTTCC CTGTGGGCCA GGGATGCTCG	1279
GTCCAGAGG AGGACCTAGT GACATCATGG GACAGGTCAA AGCATTAGGG CCACCTCCAT	1339
GGCCCCAGAC AGACTAAAGC TGCCCTCCTG GTGCAGGGCC GAGGGGACAC AAGGACCTAC	1399
CTGGAAGCAG CTGACATGCT GGTGGACGGC CGTTACTGGA GCGCGTGCCC CTCCCTCCCC	1459
GTGCTTCATG TGA CTCTTG GCTCTCTGCT GCTGCGTTGG CAGAACCCTG GGTGGGCAGG	1519
CACCCGGAGG AGGAGCAGCA GCTGTGTCAT CCTGTGCCCC CCATGTGCTG TGTGCTGTTT	1579
GCATGGCAGG GCTCCAGCTG CCTTCAGCCC TGTGACGTCT CCTCAGGGCA GCTGGACAGG	1639
CTTGGCACGG CCCGGGAAGT GCAGCAGGCA GCTTTTCTTT GGGGTGGGAC TTGCCCTGAG	1699
CTTGGAGCTG CCACCTGGAG GACTTGCTG TTCCGACTCC ACCTGTGCAG CCGGGGCCAC	1759
CCCAGGAGAA AGTGTCCAGG TGGGGGCTGG CAGTCCCTGG CTGCAG	1805

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Glu Pro Leu Phe Pro Ala Pro Phe Trp Glu Val Ile Tyr Gly Ser
1 5 10 15
His Leu Gln Gly Asn Leu Ser Leu Leu Ser Pro Asn His Ser Leu Leu
20 25 30
Pro Pro His Leu Leu Leu Asn Ala Ser His Gly Ala Phe Leu Pro Leu
35 40 45
Gly Leu Lys Val Thr Ile Val Gly Leu Tyr Leu Ala Val Cys Val Gly
50 55 60
Gly Leu Leu Gly Asn Cys Leu Val Met Tyr Val Ile Leu Arg His Thr
65 70 75 80
Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu Ala Leu Ala
85 90 95
Asp Thr Leu Val Leu Leu Thr Leu Pro Phe Gln Gly Thr Asp Ile Leu
100 105 110
Leu Gly Phe Trp Pro Phe Gly Asn Ala Leu Cys Lys Thr Val Ile Ala
115 120 125
Ile Asp Tyr Tyr Asn Met Phe Thr Ser Thr Phe Thr Leu Thr Ala Met
130 135 140
Ser Val Asp Arg Tyr Val Ala Ile Cys His Pro Ile Arg Ala Leu Asp
145 150 155 160
Val Arg Thr Ser Ser Lys Ala Gln Ala Val Asn Val Ala Ile Trp Ala
165 170 175
Leu Ala Ser Val Val Gly Val Pro Val Ala Ile Met Gly Ser Ala Gln
180 185 190
Val Glu Asp Glu Glu Ile Glu Cys Leu Val Glu Ile Pro Thr Pro Gln
195 200 205
Asp Tyr Trp Gly Pro Val Phe Ala Ile Cys Ile Phe Leu Phe Ser Phe
210 215 220
Ile Val Pro Val Leu Val Ile Ser Val Cys Tyr Ser Leu Met Ile Arg
225 230 235 240
Arg Leu Arg Gly Val Arg Leu Leu Ser Gly Ser Arg Glu Lys Asp Arg
245 250 255
Asn Leu Arg Arg Ile Thr Arg Leu Val Leu Val Val Val Ala Val Phe
260 265 270
Val Gly Cys Trp Thr Pro Val Gln Val Phe Val Leu Ala Gln Gly Leu
275 280 285
Gly Val Gln Pro Ser Ser Glu Thr Ala Val Ala Ile Leu Arg Phe Cys
290 295 300
Thr Ala Leu Gly Tyr Val Asn Ser Cys Leu Asn Pro Ile Leu Tyr Ala
305 310 315 320
Phe Leu Asp Glu Asn Phe Lys Ala Cys Phe Arg Lys Phe Cys Cys Ala
325 330 335

Ser Ala Leu Arg Arg Asp Val Gln Val Ser Asp Arg Val Arg Ser Ile
340 345 350

Ala Lys Asp Val Ala Leu Ala Cys Lys Thr Ser Glu Thr Val Pro Arg
355 360 365

Pro Ala
370

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: group(9, 12, 33, 40, 48)
- (D) OTHER INFORMATION: /note= "Extracellular Asn residues that are consensus sites for N-linked glycosylation"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	Asp	Ser	Ser	Ala	Ala	Pro	Thr	Asn	Ala	Ser	Asn	Cys	Thr	Asp	Ala	1	5	10	15
Leu	Ala	Tyr	Ser	Ser	Cys	Ser	Pro	Ala	Pro	Ser	Pro	Gly	Ser	Trp	Val	20	25	30	
Asn	Leu	Ser	His	Leu	Asp	Gly	Asn	Leu	Ser	Asp	Pro	Cys	Gly	Pro	Asn	35	40	45	
Arg	Thr	Asn	Leu	Gly	Gly	Arg	Asp	Ser	Leu	Cys	Pro	Pro	Thr	Gly	Ser	50	55	60	
Pro	Ser	Met	Ile	Thr	Ala	Ile	Thr	Ile	Met	Ala	Leu	Tyr	Ser	Ile	Val	65	70	75	80
Cys	Val	Val	Gly	Leu	Phe	Gly	Asn	Phe	Leu	Val	Met	Tyr	Val	Ile	Val	85	90	95	
Arg	Tyr	Thr	Lys	Met	Lys	Thr	Ala	Thr	Asn	Ile	Tyr	Ile	Phe	Asn	Leu	100	105	110	
Ala	Leu	Ala	Asp	Ala	Leu	Ala	Thr	Ser	Thr	Leu	Pro	Phe	Gln	Ser	Val	115	120	125	
Asn	Tyr	Leu	Met	Gly	Thr	Trp	Pro	Phe	Gly	Thr	Ile	Leu	Cys	Lys	Ile	130	135	140	
Val	Ile	Ser	Ile	Asp	Tyr	Tyr	Asn	Met	Phe	Thr	Ser	Ile	Phe	Thr	Leu	145	150	155	160
Cys	Thr	Met	Ser	Val	Asp	Arg	Tyr	Ile	Ala	Val	Cys	His	Pro	Val	Lys	165	170	175	
Ala	Leu	Asp	Phe	Arg	Thr	Pro	Arg	Asn	Ala	Lys	Ile	Ile	Asn	Val	Cys	180	185	190	
Asn	Trp	Ile	Leu	Ser	Ser	Ala	Ile	Gly	Leu	Pro	Val	Met	Phe	Met	Ala	195	200	205	

Thr	Thr	Lys	Tyr	Arg	Gln	Gly	Ser	Ile	Asp	Cys	Thr	Leu	Thr	Phe	Ser
210						215					220				
His	Pro	Thr	Trp	Tyr	Trp	Glu	Asn	Leu	Val	Lys	Ile	Cys	Val	Phe	Ile
225					230					235					240
Phe	Ala	Phe	Ile	Met	Pro	Val	Leu	Ile	Ile	Thr	Val	Cys	Tyr	Gly	Leu
				245					250					255	
Met	Ile	Leu	Arg	Leu	Lys	Ser	Val	Arg	Met	Leu	Ser	Gly	Ser	Lys	Glu
			260					265					270		
Lys	Asp	Arg	Asn	Leu	Arg	Arg	Ile	Thr	Arg	Met	Val	Leu	Val	Val	Val
		275					280					285			
Ala	Val	Phe	Ile	Val	Cys	Trp	Thr	Pro	Ile	His	Ile	Tyr	Val	Ile	Ile
	290					295					300				
Lys	Ala	Leu	Val	Thr	Ile	Pro	Glu	Thr	Thr	Phe	Gln	Thr	Val	Ser	Trp
305					310					315					320
His	Phe	Cys	Ile	Ala	Leu	Gly	Tyr	Thr	Asn	Ser	Cys	Leu	Asn	Pro	Val
			325					330						335	
Leu	Tyr	Ala	Phe	Leu	Asp	Glu	Asn	Phe	Lys	Arg	Cys	Phe	Arg	Glu	Phe
		340						345					350		
Cys	Ile	Pro	Thr	Ser	Ser	Asn	Ile	Glu	Gln	Gln	Asn	Ser	Thr	Arg	Ile
		355					360					365			
Arg	Gln	Asn	Thr	Arg	Asp	His	Pro	Ser	Thr	Ala	Asn	Thr	Val	Asp	Arg
	370					375					380				
Thr	Asn	His	Gln	Leu	Glu	Asn	Leu	Glu	Ala	Glu	Thr	Ala	Pro	Leu	Pro
385				390				395							400
Phe	Ile	Gly	Phe	Ile	Arg	Ser	Thr	Ser	Glu	Gln	Glu	Asn	Cys	Glu	
			405					410						415	

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: group(18, 33)
- (D) OTHER INFORMATION: /note= "Extracellular Asn residues that are consensus sites for N-linked glycosylation"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Glu	Pro	Ala	Pro	Ser	Ala	Gly	Ala	Glu	Leu	Gln	Pro	Pro	Leu	Phe
1				5					10					15	
Ala	Asn	Ala	Ser	Asp	Ala	Tyr	Pro	Ser	Ala	Cys	Pro	Ser	Ala	Gly	Ala
			20					25					30		
Asn	Ala	Ser	Gly	Pro	Pro	Ala	Arg	Ser	Ala	Ser	Ser	Leu	Ala	Leu	Ala
			35				40					45			

Ile	Ala	Ile	Thr	Ala	Leu	Tyr	Ser	Ala	Val	Cys	Ala	Val	Gly	Leu	Ile	50	55	60
Gly	Asn	Val	Leu	Val	Met	Phe	Gly	Ile	Val	Arg	Tyr	Thr	Lys	Met	Lys	65	70	75
Thr	Ala	Thr	Asn	Ile	Tyr	Ile	Phe	Asn	Leu	Ala	Leu	Ala	Asp	Ala	Leu	85	90	95
Ala	Thr	Ser	Thr	Leu	Pro	Phe	Gln	Ser	Ala	Lys	Tyr	Leu	Met	Glu	Thr	100	105	110
Trp	Pro	Phe	Gly	Glu	Leu	Leu	Cys	Lys	Ala	Val	Leu	Ser	Ile	Asp	Tyr	115	120	125
Tyr	Asn	Met	Phe	Thr	Ser	Ile	Phe	Thr	Leu	Thr	Met	Met	Ser	Val	Asp	130	135	140
Arg	Tyr	Ile	Ala	Val	Cys	His	Pro	Val	Lys	Ala	Leu	Asp	Phe	Arg	Thr	145	150	155
Pro	Ala	Lys	Ala	Lys	Leu	Ile	Asn	Ile	Cys	Ile	Trp	Val	Leu	Ala	Ser	165	170	175
Gly	Val	Gly	Val	Pro	Ile	Met	Val	Met	Ala	Val	Thr	Arg	Pro	Arg	Asp	180	185	190
Gly	Ala	Val	Val	Cys	Met	Leu	Gln	Phe	Pro	Ser	Pro	Ser	Trp	Tyr	Trp	195	200	205
Asp	Thr	Val	Thr	Lys	Ile	Cys	Val	Phe	Leu	Phe	Ala	Phe	Val	Val	Pro	210	215	220
Ile	Leu	Ile	Ile	Thr	Val	Cys	Tyr	Gly	Leu	Met	Leu	Leu	Arg	Leu	Arg	225	230	235
Ser	Val	Arg	Leu	Leu	Ser	Gly	Ser	Lys	Glu	Lys	Asp	Arg	Ser	Leu	Arg	245	250	255
Arg	Ile	Thr	Arg	Met	Val	Leu	Val	Val	Val	Gly	Ala	Phe	Val	Val	Cys	260	265	270
Trp	Ala	Pro	Ile	His	Ile	Phe	Val	Ile	Val	Trp	Thr	Leu	Val	Asp	Ile	275	280	285
Arg	Arg	Asp	Pro	Leu	Val	Val	Ala	Ala	Leu	His	Leu	Cys	Ile	Ala	Leu	290	295	300
Gly	Tyr	Ala	Asn	Ser	Ser	Leu	Asn	Pro	Val	Leu	Tyr	Ala	Phe	Leu	Asp	305	310	315
Glu	Asn	Phe	Lys	Arg	Cys	Phe	Arg	Gln	Leu	Cys	Arg	Lys	Pro	Cys	Gly	325	330	335
Arg	Pro	Asp	Pro	Ser	Ser	Phe	Ser	Arg	Ala	Arg	Glu	Ala	Thr	Ala	Arg	340	345	350
Glu	Arg	Val	Thr	Ala	Cys	Thr	Pro	Ser	Asp	Gly	Pro	Gly	Gly	Gly	Ala	355	360	365
Ala	Ala															370		

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: group(25, 39)
- (D) OTHER INFORMATION: /note= "Extracellular Asn residues that are consensus sites for N-linked glycosylation"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Met Glu Ser Pro Ile Gln Ile Phe Arg Gly Asp Pro Gly Pro Thr Cys
1      5      10      15
Ser Pro Ser Ala Cys Leu Leu Pro Asn Ser Ser Ser Trp Phe Pro Asn
20     25     30
Trp Ala Glu Ser Asp Ser Asn Gly Ser Val Gly Ser Glu Asp Gln Gln
35     40     45
Leu Glu Ser Ala His Ile Ser Pro Ala Ile Pro Val Ile Ile Thr Ala
50     55     60
Val Tyr Ser Val Val Phe Val Val Gly Leu Val Gly Asn Ser Leu Val
65     70     75     80
Met Phe Val Ile Ile Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile
85     90     95
Tyr Ile Phe Asn Leu Ala Leu Ala Asp Ala Leu Val Thr Thr Thr Met
100    105    110
Pro Phe Gln Ser Ala Val Tyr Leu Met Asn Ser Trp Pro Phe Gly Asp
115    120    125
Val Leu Cys Lys Ile Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr
130    135    140
Ser Ile Phe Thr Leu Thr Met Met Ser Val Asp Arg Tyr Ile Ala Val
145    150    155    160
Cys His Pro Val Lys Ala Leu Asp Phe Arg Thr Pro Leu Lys Ala Lys
165    170    175
Ile Ile Asn Ile Cys Ile Trp Leu Leu Ala Ser Ser Val Gly Ile Ser
180    185    190
Ala Ile Val Leu Gly Gly Thr Lys Val Arg Glu Asp Val Ile Glu Cys
195    200    205
Ser Leu Gln Phe Pro Asp Asp Glu Trp Trp Asp Leu Phe Met Lys Ile
210    215    220
Cys Val Phe Val Phe Ala Phe Val Ile Pro Val Leu Ile Ile Ile Val
225    230    235    240
Cys Tyr Thr Leu Met Ile Leu Arg Leu Lys Ser Val Arg Leu Leu Ser
245    250    255
Gly Ser Arg Glu Lys Asp Arg Asn Leu Arg Arg Ile Thr Lys Leu Val
260    265    270

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```

Leu Val Val Val Ala Val Phe Ile Ile Cys Trp Thr Pro Ile His Ile
  275                      280                      285

Phe Ile Leu Val Glu Ala Leu Gly Ser Thr Ser His Ser Thr Ala Ala
  290                      295                      300

Leu Ser Ser Tyr Tyr Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Ser
  305                      310                      315                      320

Leu Asn Pro Val Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys
          325                      330                      335

Phe Arg Asp Phe Cys Phe Pro Ile Lys Met Arg Met Glu Arg Gln Ser
          340                      345                      350

Thr Asn Arg Val Arg Asn Thr Val Gln Asp Pro Ala Ser Met Arg Asp
          355                      360                      365

Val Gly Gly Met Asn Lys Pro Val Glu Gln Met His Glu Lys Ser Ile
          370                      375                      380

Pro Tyr Ser Gln Glu Thr Leu Val Val Asp
  385                      390

```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: group(19, 26, 37)
- (D) OTHER INFORMATION: /note= "Extracellular Asn residues that are consensus sites for N-linked glycosylation"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```

Met Glu Pro Leu Phe Pro Ala Pro Phe Trp Ile Tyr Gly Ser His Leu
  1                      5                      10                      15

Gln Gly Asn Leu Ser Leu Leu Ser Pro Asn His Ser Leu Leu Pro Pro
          20                      25                      30

His Leu Leu Leu Asn Ala Ser His Gly Ala Leu Pro Leu Gly Leu Lys
          35                      40                      45

Val Thr Ile Val Gly Leu Tyr Leu Ala Val Cys Val Gly Gly Leu Leu
          50                      55                      60

Gly Asn Cys Leu Val Met Tyr Val Leu Leu Arg His Thr Lys Met Lys
          65                      70                      75                      80

Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu Ala Leu Ala Asp Thr Leu
          85                      90                      95

Val Leu Leu Thr Leu Pro Phe Gln Gly Thr Asp Ile Leu Leu Gly Pro
          100                      105                      110

Trp Pro Phe Gly Asn Ala Leu Cys Lys Thr Val Ile Ala Ile Asp Tyr
          115                      120                      125

```

Tyr	Asn	Met	Phe	Thr	Ser	Thr	Phe	Thr	Leu	Thr	Ala	Met	Ser	Val	Asp	130	135	140
Arg	Tyr	Val	Ala	Ile	Cys	His	Pro	Ile	Arg	Ala	Leu	Asp	Val	Arg	Thr	145	150	155
Ser	Ser	Lys	Ala	Gln	Ala	Val	Asn	Val	Ala	Ile	Trp	Ala	Leu	Ala	Ser	165	170	175
Val	Val	Gly	Val	Pro	Val	Ala	Ile	Met	Gly	Ser	Ala	Gln	Val	Glu	Asp	180	185	190
Glu	Glu	Ile	Glu	Cys	Leu	Val	Glu	Ile	Pro	Thr	Pro	Gln	Asp	Tyr	Trp	195	200	205
Gly	Pro	Val	Phe	Ala	Ile	Cys	Ile	Phe	Leu	Phe	Ser	Phe	Ile	Val	Pro	210	215	220
Val	Leu	Val	Ile	Ser	Val	Cys	Tyr	Ser	Leu	Met	Ile	Arg	Arg	Leu	Arg	225	230	235
Gly	Val	Arg	Leu	Leu	Ser	Gly	Ser	Arg	Glu	Lys	Asp	Arg	Asn	Leu	Arg	245	250	255
Arg	Ile	Thr	Arg	Leu	Val	Leu	Val	Val	Val	Ala	Val	Phe	Val	Gly	Cys	260	265	270
Trp	Thr	Pro	Val	Gln	Val	Phe	Val	Leu	Ala	Gln	Gly	Leu	Gly	Val	Gln	275	280	285
Pro	Ser	Ser	Glu	Thr	Ala	Val	Ala	Ile	Leu	Arg	Phe	Cys	Thr	Ala	Leu	290	295	300
Gly	Tyr	Val	Asn	Ser	Cys	Leu	Asn	Pro	Ile	Leu	Tyr	Ala	Phe	Leu	Asp	305	310	315
Glu	Asn	Phe	Lys	Ala	Cys	Phe	Arg	Lys	Phe	Cys	Cys	Ala	Ser	Ala	Leu	325	330	335
Arg	Arg	Asp	Val	Gln	Val	Ser	Asp	Arg	Val	Arg	Ser	Ile	Ala	Lys	Asp	340	345	350
Val	Ala	Leu	Ala	Cys	Lys	Thr	Ser	Glu	Thr	Val	Pro	Arg	Pro	Ala		355	360	365

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /note= "Extracellular Asn residue which is a consensus site for N-linked glycosylation"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Glu	Glu	Gly	Gly	Asp	Phe	Asp	Asn	Tyr	Tyr	Gly	Ala	Asp	Asn	Gln
1				5					10					15	

Ser	Glu	Cys	Glu	Tyr	Thr	Asp	Trp	Lys	Ser	Ser	Gly	Ala	Leu	Ile	Pro
		20						25					30		
Ala	Ile	Tyr	Met	Leu	Val	Phe	Leu	Leu	Gly	Thr	Thr	Gly	Asn	Gly	Leu
		35					40					45			
Val	Leu	Trp	Thr	Val	Phe	Arg	Ser	Ser	Arg	Lys	Arg	Arg	Ser	Ala	Asp
	50					55					60				
Ile	Phe	Ile	Ala	Ser	Leu	Ala	Val	Ala	Asp	Leu	Thr	Phe	Val	Val	Thr
65					70					75					80
Leu	Pro	Leu	Ala	Thr	Tyr	Thr	Tyr	Arg	Asp	Tyr	Asp	Trp	Pro	Phe	Gly
				85					90					95	
Thr	Phe	Phe	Cys	Lys	Leu	Ser	Ser	Tyr	Leu	Ile	Phe	Val	Asn	Met	Tyr
			100					105					110		
Ala	Ser	Val	Phe	Cys	Leu	Thr	Gly	Leu	Ser	Phe	Asp	Arg	Tyr	Leu	Ala
		115					120					125			
Ile	Val	Arg	Pro	Val	Ala	Asn	Ala	Arg	Leu	Arg	Leu	Arg	Val	Ser	Gly
	130					135					140				
Ala	Val	Ala	Thr	Ala	Val	Leu	Trp	Val	Leu	Ala	Ala	Leu	Leu	Ala	Met
145					150					155					160
Pro	Val	Met	Val	Leu	Thr	Thr	Gly	Asp	Leu	Glu	Asn	Thr	Thr	Val	Gln
				165					170					175	
Cys	Tyr	Met	Asp	Tyr	Ser	Ser	Ser	Glu	Trp	Ala	Trp	Glu	Val	Gly	Leu
			180					185					190		
Gly	Val	Ser	Ser	Thr	Thr	Val	Gly	Phe	Val	Val	Pro	Phe	Thr	Ile	Met
		195					200					205			
Leu	Thr	Cys	Tyr	Phe	Phe	Ile	Ala	Gln	Thr	Ile	Ala	Gly	His	Phe	Arg
	210					215					220				
Lys	Glu	Arg	Ile	Glu	Gly	Leu	Arg	Lys	Arg	Arg	Arg	Leu	Leu	Ser	Ile
225					230					235					240
Ile	Val	Val	Leu	Val	Val	Thr	Phe	Ala	Leu	Cys	Trp	Met	Pro	Tyr	His
				245					250					255	
Leu	Tyr	Met	Leu	Gly	Ser	Leu	Leu	His	Trp	Pro	Cys	Asp	Asp	Leu	Phe
			260					265					270		
Leu	Met	Asn	Ile	Phe	Pro	Tyr	Cys	Thr	Cys	Ile	Ser	Tyr	Val	Asn	Ser
		275					280					285			
Cys	Leu	Asn	Pro	Phe	Leu	Tyr	Ala	Phe	Phe	Asp	Pro	Arg	Phe	Arg	Ala
	290					295					300				
Cys	Thr	Ser	Met	Leu	Cys	Cys	Gly	Gln	Ser	Arg	Cys	Ala	Gly	Thr	Ser
305					310					315					320
His	Ser	Ser	Ser	Gly	Glu	Lys	Ser	Ala	Ser	Tyr	Ser	Ser	Gly	His	Ser
				325					330					335	
Gln	Gly	Pro	Gly	Pro	Asn	Met	Gly	Lys	Gly	Gly					
			340					345							

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "Any amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Tyr Gly Gly Phe Xaa
1 5